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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:21:25 ; Search time 388 Seconds
                                              (without alignments)
                                              303.816 Million cell updates/sec

Title: US-10-529-447-25
Perfect score: 30
Sequence: 1 cagaagacaaatcacaaacgacttcgaggg 30

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4287981 seqs, 1966746056 residues

Total number of hits satisfying chosen parameters: 8575962

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                 11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	66.7	39171	1	US-09-815-264-73839	Sequence 73839, A
	2	20	66.7	107015	1	US-09-815-264-58917	Sequence 58917, A
	3	19.4	64.7	579	6	US-10-948-737-3029	Sequence 3029, Ap
	4	19.4	64.7	579	6	US-10-948-737-11344	Sequence 11344, A
	5	19.4	64.7	1000	8	US-11-266-748A-406210	Sequence 406210,
c	6	19.4	64.7	1000	8	US-11-266-748A-477256	Sequence 477256,

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:04:29 ; Search time 1087 Seconds
                                              (without alignments)
                                 339.182 Million cell updates/sec

Title: US-10-529-447-25
Perfect score: 30
Sequence: 1 cagaagacaaatcacaaacgacttcgaggg 30

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score Match Length DB ID   Description
----
    1   21.8   72.7   3827 16 US-11-136-527-3202   Sequence 3202, Ap

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:50:15 ; Search time 194 Seconds
                                        (without alignments)
                               289.211 Million cell updates/sec

Title: US-10-529-447-25
Perfect score: 30
Sequence: 1 cagaagacaaatcacaaacgacttcgaggg 30

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database·:   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19.2	64.0	11120	3	US-09-201-227A-7	Sequence 7, Appli
c	2	18.8	62.7	601	3	US-09-949-016-204965	Sequence 204965,
c	3	18.8	62.7	601	3	US-09-949-016-204966	Sequence 204966,
c	4	18.8	62.7	601	3	US-09-949-016-204967	Sequence 204967,
c	5	18.8	62.7	2601	3	US-09-291-922-7	Sequence 7, Appli
c	6	18.8	62.7	79756	3	US-09-949-016-17537	Sequence 17537, A
c	7	18.8	62.7	139049	3	US-09-949-016-17030	Sequence 17030, A

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:02:56 ; Search time 4142 Seconds
                                        (without alignments)
                                        449.326 Million cell updates/sec

Title: US-10-529-447-25
Perfect score: 30
Sequence: 1 cagaagacaaatcacaaacgacttcgaggg 30

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_est13:*
                12: gb_est12:*
                13: gb_est11:*
                14: gb_est10:*
                15: gb_gss1:*
                16: gb_gss2:*
                17: gb_gss3:*
                18: gb_gss4:*
                19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:00:30 ; Search time 1492 Seconds
                                              (without alignments)
                                              1389.353 Million cell updates/sec

Title: US-10-529-447-25
Perfect score: 30
Sequence: 1 cagaagacaaatcacaaacgacttcgaggg 30

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30	100.0	30	2	DD309757	DD309757 Method an
2	30	100.0	7851	10	PPH35CG	M74117 Human papil

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 08:36:00 ; Search time 514 Seconds
                                           (without alignments)
                                 432.830 Million cell updates/sec

Title: US-10-529-447-25
Perfect score: 30
Sequence: 1 cagaagacaaatcacaaacgacttcgaggg 30

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
    1   30   100.0   30   12   ADM82974   Adm82974 Human pap

```
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OM nucleic - nucleic search, using sw model

Run on:          February  8, 2007, 10:21:25 ; Search time 285 Seconds
                                            (without alignments)
                                 303.816 Million cell updates/sec


Title:          US-10-529-447-21
Perfect score:  22
Sequence:       1 ccagctggacaagcagaaccgg 22


Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0


Searched:       4287981 seqs, 1966746056 residues


Total number of hits satisfying chosen parameters:     8575962


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries


Database :      Published_Applications_NA_New:*
                1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                6:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                7:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                8:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                9:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                10:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                11:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*


       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.


                            SUMMARIES
                %
Result          Query
   No.   Score  Match Length DB  ID                         Description
------------------------------------------------------------------------------
        1     22  100.0     39  10  US-11-358-285-15           Sequence 15, Appl
        2     22  100.0    276   6  US-10-512-045A-2           Sequence 2, Appli
        3     22  100.0    279   6  US-10-512-190-1            Sequence 1, Appli
        4     22  100.0    294   6  US-10-511-814-9            Sequence 9, Appli
        5     22  100.0    294   6  US-10-511-814-10           Sequence 10, Appl
        6     22  100.0    294   6  US-10-511-814-12           Sequence 12, Appl
```

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:04:29 ; Search time 797 Seconds
                                           (without alignments)
                                           339.182 Million cell updates/sec

Title: US-10-529-447-21
Perfect score: 22
Sequence: 1 ccagctggacaagcagaaccgg 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
        1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
        2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
        3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
        4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
        5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
        6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
        7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
        8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
        9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
       10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
       11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
       12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
       13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
       14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
       15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
       16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   22 100.0   39 3 US-09-820-765-15   Sequence 15, Appl

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:50:15 ; Search time 142 Seconds
                                        (without alignments)
                                 289.211 Million cell updates/sec

Title: US-10-529-447-21
Perfect score: 22
Sequence: 1 ccagctggacaagcagaaccgg 22

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Issued_Patents_NA:*
         1:   /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
         2:   /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
         3:   /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
         4:   /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
         5:   /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
         6:   /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
         7:   /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
         8:   /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
         9:   /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
         10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	39	3	US-08-944-368A-15	Sequence 15, Appl
2	22	100.0	39	3	US-09-820-764-15	Sequence 15, Appl
3	22	100.0	39	3	US-09-986-118A-15	Sequence 15, Appl
4	22	100.0	39	3	US-09-824-017-15	Sequence 15, Appl
5	22	100.0	294	3	US-09-430-201-7	Sequence 7, Appli
6	22	100.0	297	2	US-08-406-248-5	Sequence 5, Appli
7	22	100.0	297	3	US-08-944-368A-3	Sequence 3, Appli

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:02:56 ; Search time 3038 Seconds
                                          (without alignments)
                                          449.326 Million cell updates/sec

Title: US-10-529-447-21
Perfect score: 22
Sequence: 1 ccagctggacaagcagaaccgg 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query

```
                    GenCore version 6.2
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OM nucleic - nucleic search, using sw model

Run on:          February  8, 2007, 09:00:30 ; Search time 1094 Seconds
                                          (without alignments)
                                 1389.353 Million cell updates/sec

Title:          US-10-529-447-21
Perfect score:  22
Sequence:       1 ccagctggacaagcagaaccgg 22

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters:      15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :      GenEmbl:*
                1:  gb_env:*
                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
                6:  gb_ro:*
                7:  gb_sts:*
                8:  gb_sy:*
                9:  gb_un:*
               10:  gb_vi:*
               11:  gb_ov:*
               12:  gb_htg:*
               13:  gb_in:*
               14:  gb_om:*
               15:  gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	2	DD309753	DD309753 Method an
2	22	100.0	37	2	BD234788	BD234788 Polypepti

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 08:36:00 ;. Search time 377 Seconds
                                               (without alignments)
                                               432.830 Million cell updates/sec

Title: US-10-529-447-21
Perfect score: 22
Sequence: 1 ccagctggacaagcagaaccgg 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
                 1:   geneseqn1980s:*
                 2:   geneseqn1990s:*
                 3:   geneseqn2000s:*
                 4:   geneseqn2001as:*
                 5:   geneseqn2001bs:*
                 6:   geneseqn2002as:*
                 7:   geneseqn2002bs:*
                 8:   geneseqn2003as:*
                 9:   geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   22   100.0   22 12   ADM82969   Adm82969 Human pap

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:21:25 ; Search time 233 Seconds
                                            (without alignments)
                                            303.816 Million cell updates/sec

Title: US-10-529-447-10
Perfect score: 18
Sequence: 1 agtcgcactcgcttggtg 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4287981 seqs, 1966746056 residues

Total number of hits satisfying chosen parameters: 8575962

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                 11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	15.4	85.6	703	6	US-10-956-160-10277	Sequence 10277, A
c 2	15.4	85.6	703	6	US-10-956-160-220384	Sequence 220384,
c 3	15	83.3	124122	1	US-09-815-264-67000	Sequence 67000, A
4	14.8	82.2	605	6	US-10-488-619-2773	Sequence 2773, Ap
5	14.8	82.2	799	8	US-11-266-748A-77315	Sequence 77315, A
6	14.8	82.2	799	8	US-11-266-748A-109776	Sequence 109776,

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:04:29 ; Search time 652 Seconds
                                          (without alignments)
                                          339.182 Million cell updates/sec

Title: US-10-529-447-10
Perfect score: 18
Sequence: 1 agtcgcactcgcttggtg 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
                1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB ID   Description
----
  c   1   16   88.9   938 3   US-09-728-552-16   Sequence 16, Appl

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:50:15 ; Search time 116 Seconds
                                             (without alignments)
                                             289.211 Million cell updates/sec

Title: US-10-529-447-10
Perfect score: 18
Sequence: 1 agtcgcactcgcttggtg 18

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Issued_Patents_NA:*
                  1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                  2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                  3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                  4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                  5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                  6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                  7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                  8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                  9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                  10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	16	88.9	938	3	US-09-078-294-16	Sequence 16, Appl
c	2	14.8	82.2	594	3	US-09-533-559-1249	Sequence 1249, Ap
c	3	14.8	82.2	301828	3	US-09-949-016-13969	Sequence 13969, A
	4	14.8	82.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	5	14.8	82.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	6	14.4	80.0	601	3	US-09-949-016-71238	Sequence 71238, A
	7	14.4	80.0	3074	3	US-09-710-279-3770	Sequence 3770, Ap

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:02:56 ; Search time 2485 Seconds
                                         (without alignments)
                                 449.326 Million cell updates/sec

Title: US-10-529-447-10
Perfect score: 18
Sequence: 1 agtcgcactcgcttggtg 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:00:30 ; Search time 896 Seconds
                                        (without alignments)
                                        1389.353 Million cell updates/sec

Title: US-10-529-447-10
Perfect score: 18
Sequence: 1 agtcgcactcgcttggtg 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	2	DD309742	DD309742 Method an
c 2	18	100.0	7851	10	PPH35CG	M74117 Human papil

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 08:36:00 ; Search time 308 Seconds
                                            (without alignments)
                                            432.830 Million cell updates/sec

Title: US-10-529-447-10
Perfect score: 18
Sequence: 1 agtcgcactcgcttggtg 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                            SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   18   100.0   18   12   ADM82960   Adm82960 Human pap

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:21:25 ; Search time 233 Seconds
                                              (without alignments)
                                              303.816 Million cell updates/sec

Title: US-10-529-447-9
Perfect score: 18
Sequence: 1 accaaagcctgctccgtg 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4287981 seqs, 1966746056 residues

Total number of hits satisfying chosen parameters: 8575962

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_New:*
                1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
        ----
        1   16.4   91.1 80276   6   US-10-669-920-258   Sequence 258, App
   c   2   16   88.9   478   8   US-11-266-748A-428049   Sequence 428049,
        3   15.4   85.6   386   8   US-11-266-748A-103625   Sequence 103625,
   c   4   15.4   85.6   386   8   US-11-266-748A-156436   Sequence 156436,
        5   15.4   85.6   789   6   US-10-419-128-4625   Sequence 4625, Ap
        6   15.4   85.6   840   6   US-10-419-128-4527   Sequence 4527, Ap

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:04:29 ; Search time 652 Seconds
                                              (without alignments)
                                  339.182 Million cell updates/sec

Title: US-10-529-447-9
Perfect score: 18
Sequence: 1 accaaagcctgctccgtg 18

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
       1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
       2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
       3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
       4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
       5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/ÜS09C_PUBCOMB.seq:*
       6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
       7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
       8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
       9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
      10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
      11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
      12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
      13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
      14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
      15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
      16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16.4	91.1	78028	7	US-10-034-650-37	Sequence 37, Appl

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:50:15 ; Search time 116 Seconds
                                           (without alignments)
                                    289.211 Million cell updates/sec

Title: US-10-529-447-9
Perfect score: 18
Sequence: 1 accaaagcctgctccgtg 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Issued_Patents_NA:*
          1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
          2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
          3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
          4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
          5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
          6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
          7:. /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
          8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
          9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
          10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	16.4	91.1	285986	3	US-09-949-016-12287	Sequence 12287, A
2	15.4	85.6	20	3	US-09-658-679A-56	Sequence 56, Appl
3	15.4	85.6	641	3	US-09-533-559-6370	Sequence 6370, Ap
4	15.4	85.6	789	3	US-09-252-991A-4625	Sequence 4625, Ap
5	15.4	85.6	840	3	US-09-252-991A-4527	Sequence 4527, Ap
6	15.4	85.6	1002	3	US-09-252-991A-4423	Sequence 4423, Ap
c 7	15.4	85.6	1164	3	US-09-252-991A-4249	Sequence 4249, Ap

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:02:56 ; Search time 2485 Seconds
                                            (without alignments)
                                            449.326 Million cell updates/sec

Title: US-10-529-447-9
Perfect score: 18
Sequence: 1 accaaagcctgctccgtg 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                        %
Result   Query

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:00:30 ; Search time 896 Seconds
                                        (without alignments)
                                 1389.353 Million cell updates/sec

Title: US-10-529-447-9
Perfect score: 18
Sequence: 1 accaaagcctgctccgtg 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                10: gb_vi:*
                11: gb_ov:*
                12: gb_htg:*
                13: gb_in:*
                14: gb_om:*
                15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	2	DD309741	DD309741 Method an
2	18	100.0	7851	10	PPH35CG	M74117 Human papil

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 08:36:00 ; Search time 308 Seconds
                                          (without alignments)
                                          432.830 Million cell updates/sec

Title: US-10-529-447-9
Perfect score: 18
Sequence: 1 accaaagcctgctccgtg 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
                 1:   geneseqn1980s:*
                 2:   geneseqn1990s:*
                 3:   geneseqn2000s:*
                 4:   geneseqn2001as:*
                 5:   geneseqn2001bs:*
                 6:   geneseqn2002as:*
                 7:   geneseqn2002bs:*
                 8:   geneseqn2003as:*
                 9:   geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score Match Length DB   ID   Description
----
    1   18   100.0   18 12   ADM82959   Adm82959 Human pap

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:21:25 ; Search time 298 Seconds
                                    (without alignments)
                                    303.816 Million cell updates/sec

Title: US-10-529-447-2
Perfect score: 23
Sequence: 1 ggttacaatattgtaatgggctc 23

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4287981 seqs, 1966746056 residues

Total number of hits satisfying chosen parameters: 8575962

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_New:*
                1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
  c 1   23   100.0   36   7   US-11-085-749A-312   Sequence 312, App
     2   23   100.0   36   7   US-11-085-749A-313   Sequence 313, App
     3   23   100.0   54 10   US-11-358-285-26   Sequence 26, Appl
     4   23   100.0   69 10   US-11-358-285-27   Sequence 27, Appl
  c 5   23   100.0   276   6   US-10-512-045A-2   Sequence 2, Appli
  c 6   23   100.0   279   6   US-10-512-190-1   Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:04:29 ; Search time 833 Seconds
                                          (without alignments)
                                 339.182 Million cell updates/sec

Title: US-10-529-447-2
Perfect score: 23
Sequence: 1 ggttacaatattgtaatgggctc 23

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
        1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
        2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
        3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
        4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
        5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
        6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
        7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
        8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
        9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
        10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
        11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
        12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
        13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
        14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
        15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
        16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES

             %
Result   Query
   No.   Score Match Length DB ID   Description
----
 c   1   23 100.0   51 9 US-10-858-384-15   Sequence 15, Appl

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:50:15 ; Search time 149 Seconds
                                             (without alignments)
                                 289.211 Million cell updates/sec

Title: US-10-529-447-2
Perfect score: 23
Sequence: 1 ggttacaatattgtaatgggctc 23

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	23	100.0	51	3	US-09-980-523A-15	Sequence 15, Appl
	2	23	100.0	54	3	US-08-944-368A-26	Sequence 26, Appl
	3	23	100.0	54	3	US-09-820-764-26	Sequence 26, Appl
	4	23	100.0	54	3	US-09-986-118A-26	Sequence 26, Appl
	5	23	100.0	54	3	US-09-824-017-26	Sequence 26, Appl
	6	23	100.0	54	3	US-09-667-556-10	Sequence 10, Appl
	7	23	100.0	69	3	US-08-944-368A-27	Sequence 27, Appl

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:02:56 ; Search time 3176 Seconds
                                            (without alignments)
                                            449.326 Million cell updates/sec

Title: US-10-529-447-2
Perfect score: 23
Sequence: 1 ggttacaatattgtaatgggctc 23

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_est13:*
                12: gb_est12:*
                13: gb_est11:*
                14: gb_est10:*
                15: gb_gss1:*
                16: gb_gss2:*
                17: gb_gss3:*
                18: gb_gss4:*
                19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:00:30 ; Search time 1144 Seconds
                                      (without alignments)
                                 1389.353 Million cell updates/sec

Title: US-10-529-447-2
Perfect score: 23
Sequence: 1 ggttacaatattgtaatgggctc 23

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
    No.   Score Match Length DB ID   Description
    ----
      1   23   100.0   23   2   DD309734   DD309734 Method an
 c   2   23   100.0   36   2   A66389   A66389 Sequence 31

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 08:36:00 ; Search time 394 Seconds
                                          (without alignments)
                                          432.830 Million cell updates/sec

Title: US-10-529-447-2
Perfect score: 23
Sequence: 1 ggttacaatattgtaatgggctc 23

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
    1   23   100.0   23   12   ADM82953   Adm82953 Human pap

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:21:25 ; Search time 272 Seconds
                                            (without alignments)
                                            303.816 Million cell updates/sec

Title: US-10-529-447-1
Perfect score: 21
Sequence: 1 agctcagaggaggaggatgaa 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4287981 seqs, 1966746056 residues

Total number of hits satisfying chosen parameters: 8575962

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                 11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	276	6	US-10-512-045A-2	Sequence 2, Appli
2	21	100.0	279	6	US-10-512-190-1	Sequence 1, Appli
3	21	100.0	294	6	US-10-511-814-9	Sequence 9, Appli
4	21	100.0	294	6	US-10-511-814-10	Sequence 10, Appl
5	21	100.0	294	6	US-10-511-814-12	Sequence 12, Appl
6	21	100.0	294	6	US-10-511-814-13	Sequence 13, Appl

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 10:04:29 ; Search time 761 Seconds
                                      (without alignments)
                                      339.182 Million cell updates/sec

Title: US-10-529-447-1
Perfect score: 21
Sequence: 1 agctcagaggaggaggatgaa 21

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
          1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
          2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
          3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
          4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
          5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
          6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
          7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
          8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
          9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
          10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
          11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
          12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
          13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
          14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
          15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
          16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result   %
             Query
  No.   Score Match Length DB ID   .   Description
----
    1   21 100.0   271 9 US-10-357-930-62076   Sequence 62076, A

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:50:15 ; Search time 136 Seconds
                                         (without alignments)
                                 289.211 Million cell updates/sec

Title: US-10-529-447-1
Perfect score: 21
Sequence: 1 agctcagaggaggaggatgaa 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                SUMMARIES

               %
Result   Query
  No.   Score Match Length DB ID   Description
       ----
       1   21 100.0   294 3   US-09-430-201-7   Sequence 7, Appli
       2   21 100.0   297 2   US-08-406-248-5   Sequence 5, Appli
       3   21 100.0   297 3   US-08-944-368A-3   Sequence 3, Appli
       4   21 100.0   297 3   US-09-056-105-30   Sequence 30, Appl
       5   21 100.0   297 3   US-09-820-764-3   Sequence 3, Appli
       6   21 100.0   297 3   US-09-613-303-7   Sequence 7, Appli
       7   21 100.0   297 3   US-09-986-118A-3   Sequence 3, Appli

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:02:56 ; Search time 2900 Seconds
                                              (without alignments)
                                              449.326 Million cell updates/sec

Title: US-10-529-447-1
Perfect score: 21
Sequence: 1 agctcagaggaggaggatgaa 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 09:00:30 ; Search time 1045 Seconds
                                               (without alignments)
                                               1389.353 Million cell updates/sec

Title: US-10-529-447-1
Perfect score: 21
Sequence: 1 agctcagaggaggaggatgaa 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES

                         %
Result   Query
   No.   Score Match Length DB ID   Description
----
      1   21 100.0   21 2 DD309733   DD309733 Method an
      2   21 100.0   271 2 CQ530209   CQ530209 Sequence

GenCore version 6.2
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2007, 08:36:00 ; Search time 360 Seconds
                                              (without alignments)
                                              432.830 Million cell updates/sec

Title: US-10-529-447-1
Perfect score: 21
Sequence: 1 agctcagaggaggaggatgaa 21

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
           1: geneseqn1980s:*
           2: geneseqn1990s:*
           3: geneseqn2000s:*
           4: geneseqn2001as:*
           5: geneseqn2001bs:*
           6: geneseqn2002as:*
           7: geneseqn2002bs:*
           8: geneseqn2003as:*
           9: geneseqn2003bs:*
           10: geneseqn2003cs:*
           11: geneseqn2003ds:*
           12: geneseqn2004as:*
           13: geneseqn2004bs:*
           14: geneseqn2005s:*
           15: geneseqn2006s:*
           16: geneseqn2007s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
    1   21   100.0   21 12   ADM82952   Adm82952 Human pap